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Supplementary Table S1B

Filtered and combined VPS29 interactome

We filtered each of the two VPS29 interactomes, obtained by experimental replication and presented in Supplementary Tables S1 and S2, by excluding proteins that did not fulfil the following criteria: more than 1 peptide detected, a Medium/Light ratio of at least 4, a Medium/Light Count of more than 1 unless more than 2 peptides were detected.
We combined the resulting two lists of remaining proteins into one list, presented below, by excluding all proteins that did not occur in both lists. The list includes the means of each numerical parameter quantified.
Parameter definitions:
Accession: Uniprot accession number of the protein
Coverage: Percentage of protein sequence covered by identified peptides
 # Peptide Spectrum Matches (PSMs): Total number of peptides identified (including multiples of same peptide sequence)
 # Peptides: Total number of unique peptides identified (multiples of same peptide sequence count as single peptide)
 # AAs: Number of amino acids in the protein
[kDa]: Mass of the protein
calc. pI: Calculated isoelectric point of the protein
Score: Combines several parameters; a high score generally indicates high protein abundance and a high confidence of the software in the detection and quantification.
Medium/Light: Ratio of the quantification values of the medium (GFP-VPS29) and light (GFP) quantification channels
Medium/Light Count: Number of peptides quantified used to calculate Medium/Light ratio
Medium/Light Variability (%): Variability of the protein ratios used to calculate the Medium/Light ratio
Description: Name of the protein

Accession	Coverage			# PSMs			# Peptides			# AAs	MW [kDa]	calc. pI	Score			Area			Medium/Light			Medium/Light Count			Medium/Light Variability [%]			Description
	1	2	Mean	1	2	Mean	1	2	Mean				1	2	Mean	1	2	Mean	1	2	Mean	1	2	Mean	1	2	Mean	
A8K9U1	8.07	12.72	10.40	13	23	18	13	19	16	1698	191.0	5.96	63.92	105.95	84.94	2.146E6	3.319E7	1.767E7	100.000	48.694	74.347	10	15	13	0.0	145.7	72.8	cDNA FLJ76468, highly similar to Homo sapiens cullin 7 (CUL7), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9U1_HUMAN]
A9QQ22	28.78	28.54	28.66	51	25	38	12	10	11	410	43.8	5.58	189.22	96.36	142.79	2.698E8	4.440E8	3.569E8	100.000	44.373	72.187	11	4	8	0.0	22.1	11.1	Actin nucleation promoting factor (Fragment) OS=Homo sapiens GN=WASH PE=4 SV=1 - [A9QQ22_HUMAN]
B1AK87	59.23	49.62	54.43	53	26	39.5	17	12	14.5	260	29.3	6.92	215.98	100.31	158.14	3.224E8	6.246E8	4.735E8	100.000	14.676	57.338	41	14	28	0.0	51.8	25.9	Capping protein (Actin filament) muscle Z-line, beta OS=Homo sapiens GN=CAPZB PE=4 SV=1 - [B1AK87_HUMAN]
B4DF48	44.97	26.78	35.88	84	58	71	40	24	32	1023	111.7	5.80	357.92	226.75	292.33	2.000E8	3.703E8	2.851E8	100.000	100.000	100.000	4	3	4	0.0	0.0	0.0	cDNA FLJ61221, highly similar to Protein FAM21C OS=Homo sapiens PE=2 SV=1 - [B4DF48_HUMAN]

B4DP21	17.69	24.62	21.16	3	3	3	3	3	3	130	14.9	4.77	10.08	10.86	10.47	2.888E6	9.887E6	6.388E6	10.558	8.729	9.644	2	3	3	47.6	48.2	47.9	Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=2 SV=1 - [B4DP21_HUMAN]
B7Z254	7.09	21.51	14.30	3	13	8	2	6	4	437	47.8	5.08	12.54	47.32	29.93	8.296E6	7.352E7	4.091E7	23.054	78.838	50.946	2	11	7	1061.1	36.4	548.8	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=2 SV=1 - [B7Z254_HUMAN]
B7ZKT9	44.29	25.64	34.97	133	86	109.5	52	29	40.5	1174	136.4	7.44	535.80	351.17	443.49	4.800E8	9.067E8	6.933E8	100.000	100.000	100.000	102	59	81	0.0	0.0	0.0	KIAA1033 protein OS=Homo sapiens GN=KIAA1033 PE=2 SV=1 - [B7ZKT9_HUMAN]
C4AMC7	28.29	28.08	28.19	55	28	41.5	15	12	13.5	463	50.0	5.49	223.29	112.67	167.98	3.238E8	4.645E8	3.942E8	100.000	100.000	100.000	18	10	14	0.0	0.0	0.0	Putative WAS protein family homolog 3 OS=Homo sapiens GN=WASH3P PE=2 SV=2 - [WASH3_HUMAN]
D6RJ90	51.06	59.04	55.05	19	13	16	14	9	11.5	188	21.5	6.54	73.58	44.83	59.21	5.627E7	2.394E8	1.479E8	100.000	100.000	100.000	15	9	12	0.0	0.0	0.0	COMM domain containing 10, isoform CRA_b OS=Homo sapiens GN=COMMD10 PE=4 SV=1 - [D6RJ90_HUMAN]
F5GZ97	40.41	30.05	35.23	28	11	19.5	6	4	5	193	21.0	4.46	109.44	40.47	74.96	2.260E8	2.278E8	2.269E8	100.000	100.000	100.000	1	1	1	0.0		0.0	WASH complex subunit CCDC53 OS=Homo sapiens GN=CCDC53 PE=4 SV=1 - [F5GZ97_HUMAN]
F8W9X7	52.54	39.68	46.11	113	52	82.5	41	27	34	630	73.0	7.99	481.90	215.42	348.66	4.034E8	6.696E8	5.365E8	100.000	100.000	100.000	93	39	66	0.0	0.0	0.0	Coiled-coil domain-containing protein 93 OS=Homo sapiens GN=CCDC93 PE=4 SV=1 - [F8W9X7_HUMAN]
H0YN26	36.72	23.16	29.94	11	6	8.5	6	4	5	177	20.0	4.58	45.01	18.99	32.00	2.701E7	7.329E7	5.015E7	100.000	8.491	54.245	3	1	2	0.0		0.0	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=4 SV=1 - [H0YN26_HUMAN]
H3BLV8	67.34	63.32	65.33	237	242	239.5	17	17	17	199	22.3	7.62	1066.35	1104.04	1085.20	2.729E10	5.906E10	4.318E10	100.000	100.000	100.000	92	69	81	0.0	0.0	0.0	Vacuolar protein sorting-associated protein 29 (Fragment) OS=Homo sapiens GN=VPS29 PE=4 SV=1 - [H3BLV8_HUMAN]
K7EKL3	11.60	10.82	11.21	4	3	3.5	4	3	3.5	388	41.3	6.52	15.87	16.80	16.34	5.305E6	1.131E7	8.307E6	100.000	14.332	57.166	3	2	3	0.0	6328.5	3164.3	Paragranulin (Fragment) OS=Homo sapiens GN=GRN PE=4 SV=1 - [K7EKL3_HUMAN]
O60826	70.33	55.18	62.76	135	84	109.5	41	26	33.5	627	70.7	6.74	547.65	323.43	435.54	5.072E8	5.755E8	5.413E8	100.000	100.000	100.000	97	48	73	0.0	0.0	0.0	Coiled-coil domain-containing protein 22 OS=Homo sapiens GN=CCDC22 PE=1 SV=1 - [CCD22_HUMAN]
O75436	79.51	60.86	70.19	193	139	166	31	20	25.5	327	38.1	6.57	776.77	529.42	653.10	4.515E9	7.324E9	5.920E9	100.000	100.000	100.000	51	31	41	0.0	0.0	0.0	Vacuolar protein sorting-associated protein 26A OS=Homo sapiens

																												GN=VPS26A PE=1 SV=2 - [VP26A_HUMAN]
P07996	5.13	19.57	12.35	6	26	16	5	16	10.5	1170	129.3	4.94	22.96	89.35	56.16	3.113E5	2.358E7	1.195E7	100.000	4.750	52.375	3	16	10	0.0	64.6	32.3	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2 - [TSP1_HUMAN]
P13489	17.79	14.53	16.16	9	5	7	6	5	5.5	461	49.9	4.82	31.67	17.19	24.43	9.297E6	2.166E7	1.548E7	4.670	4.331	4.501	6	4	5	19.5	21.8	20.6	Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 - [RINI_HUMAN]
P13667	17.83	11.16	14.50	13	6	9.5	12	6	9	645	72.9	5.07	44.99	18.04	31.51	1.952E6	1.440E7	8.178E6	7.908	5.719	6.814	7	5	6	6.0	50.6	28.3	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN]
P14314	18.75	10.61	14.68	9	5	7	8	5	6.5	528	59.4	4.41	30.69	18.26	24.48	5.222E6	1.906E7	1.214E7	6.856	7.381	7.118	7	5	6	9.9	53.8	31.8	Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2 - [GLU2B_HUMAN]
P20020	11.92	11.37	11.65	19	13	16	12	12	12	1258	138.7	6.04	87.53	55.53	71.53	2.681E6	2.312E7	1.290E7	100.000	4.595	52.298	5	3	4	0.0	6.1	3.1	Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3 - [AT2B1_HUMAN]
P47755	69.93	67.13	68.53	43	31	37	15	13	14	286	32.9	5.85	182.02	129.15	155.59	4.477E8	7.385E8	5.931E8	100.000	100.000	100.000	30	18	24	0.0	0.0	0.0	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3 - [CAZA2_HUMAN]
P52294	19.33	10.22	14.78	8	4	6	8	4	6	538	60.2	5.01	25.63	15.04	20.33	2.014E6	7.736E6	4.875E6	7.310	26.654	16.982	2	2	2	16.1	675.8	345.9	Importin subunit alpha-1 OS=Homo sapiens GN=KPNA1 PE=1 SV=3 - [IMA1_HUMAN]
P52907	67.83	66.43	67.13	50	27	38.5	15	13	14	286	32.9	5.69	233.77	123.34	178.55	5.492E8	8.815E8	7.154E8	100.000	100.000	100.000	35	15	25	0.0	0.0	0.0	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3 - [CAZA1_HUMAN]
P68371	66.07	64.72	65.40	92	73	82.5	25	21	23	445	49.8	4.89	337.83	276.49	307.16	1.875E8	3.056E8	2.466E8	4.843	4.909	4.876	3	2	3	45.3	0.7	23.0	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
Q01105	34.14	30.34	32.24	15	14	14.5	9	7	8	290	33.5	4.32	54.13	45.79	49.96	3.854E7	1.031E8	7.082E7	5.030	5.369	5.200	12	11	12	15.6	18.2	16.9	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]
Q05DG7	36.78	36.78	36.78	25	34	29.5	4	4	4	87	9.9	5.33	141.58	155.35	148.47	9.563E9	2.214E10	1.585E10	100.000	100.000	100.000	1	1	1	0.0		0.0	VPS29 protein OS=Homo sapiens GN=VPS29 PE=2 SV=1 - [Q05DG7_HUMAN]
Q12768	46.85	37.96	42.41	161	116	138.5	51	39	45	1159	134.2	6.98	635.26	460.14	547.70	3.501E8	7.661E8	5.581E8	100.000	100.000	100.000	119	78	99	0.0	0.0	0.0	WASH complex subunit strumpellin OS=Homo sapiens GN=KIAA0196 PE=1 SV=1 - [STRUM_HUMAN]
Q13509	55.56	48.44	52.00	69	49	59	22	16	19	450	50.4	4.93	262.31	193.01	227.66	1.631E8	2.705E8	2.168E8	17.381	100.000	58.690	6	5	6	60.3	0.0	30.2	Tubulin beta-3 chain OS=Homo sapiens

																											GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]
Q13563	7.44	9.50	8.47	9	8	8.5	7	8	7.5	968	109.6	5.69	45.90	26.30	36.10	2.075E6	1.462E7	8.349E6	100.000	6.950	53.475	6	4	5	0.0	9.5	4.7	Polycystin-2 OS=Homo sapiens GN=PKD2 PE=1 SV=3 - [PKD2_HUMAN]
Q4G0F5	74.11	58.33	66.22	111	54	82.5	26	18	22	336	39.1	7.36	393.06	219.11	306.09	8.310E8	1.993E9	1.412E9	100.000	82.900	91.450	72	28	50	0.0	28.4	14.2	Vacuolar protein sorting-associated protein 26B OS=Homo sapiens GN=VPS26B PE=1 SV=2 - [VP26B_HUMAN]
Q53GA7	51.22	47.66	49.44	41	39	40	19	15	17	449	49.8	5.14	164.55	139.97	152.26	2.281E8	4.253E8	3.267E8	5.269	4.517	4.893	1	1	1	0.0		0.0	Tubulin alpha 6 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GA7_HUMAN]
Q53Q75	29.79	15.96	22.88	8	3	5.5	4	2	3	94	10.5	9.89	33.67	11.17	22.42	1.449E8	1.192E8	1.321E8	97.237	55.180	76.208	6	2	4	4.2	108.4	56.3	Putative uncharacterized protein C2orf5 (Fragment) OS=Homo sapiens GN=C2orf5 PE=2 SV=1 - [Q53Q75_HUMAN]
Q561V4	57.99	36.69	47.34	11	7	9	9	5	7	169	19.1	6.28	70.98	31.36	51.17	9.825E7	1.050E8	1.016E8	100.000	100.000	100.000	9	6	8	0.0	0.0	0.0	COMMD2 protein OS=Homo sapiens GN=COMMD2 PE=2 SV=1 - [Q561V4_HUMAN]
Q5T1M5	42.66	29.29	35.98	111	62	86.5	47	29	38	1219	133.5	5.20	452.81	247.31	350.06	1.516E8	1.865E8	1.690E8	100.000	100.000	100.000	91	49	70	0.0	0.0	0.0	FK506-binding protein 15 OS=Homo sapiens GN=FKBP15 PE=1 SV=2 - [FKB15_HUMAN]
Q6P1L8	11.03	16.55	13.79	3	2	2.5	2	2	2	145	15.9	10.24	7.84	8.99	8.42	8.218E5	6.622E6	3.722E6	13.257	11.460	12.358	2	2	2	8889.9	17375.7	13132.8	39S ribosomal protein L14, mitochondrial OS=Homo sapiens GN=MRPL14 PE=1 SV=1 - [RM14_HUMAN]
Q7Z3J2	46.00	39.04	42.52	135	105	120	44	35	39.5	963	109.5	7.21	603.17	426.87	515.02	3.794E8	6.668E8	5.231E8	100.000	100.000	100.000	110	70	90	0.0	0.0	0.0	UPF0505 protein C16orf62 OS=Homo sapiens GN=C16orf62 PE=1 SV=2 - [CP062_HUMAN]
Q7Z4G1	56.47	42.35	49.41	7	4	5.5	5	4	4.5	85	9.6	6.00	24.06	15.91	19.99	2.908E7	2.683E7	2.796E7	79.717	88.841	84.279	6	4	5	34.6	17.7	26.1	COMM domain-containing protein 6 OS=Homo sapiens GN=COMMD6 PE=1 SV=1 - [COMD6_HUMAN]
Q86VX2	42.50	33.50	38.00	21	12	16.5	10	5	7.5	200	22.5	5.92	70.26	41.67	55.96	1.240E8	1.389E8	1.315E8	100.000	100.000	100.000	14	10	12	0.0	0.0	0.0	COMM domain-containing protein 7 OS=Homo sapiens GN=COMMD7 PE=1 SV=2 - [COMD7_HUMAN]
Q8N3Y1	10.37	12.21	11.29	5	6	5.5	5	6	5.5	598	67.4	5.67	17.97	17.81	17.89	1.525E6	2.135E7	1.144E7	100.000	100.000	100.000	4	5	5	0.0	0.0	0.0	F-box/WD repeat-containing protein 8 OS=Homo sapiens GN=FBXW8 PE=1 SV=2 - [FBXW8_HUMAN]
Q8N961	6.79	5.96	6.38	7	4	5.5	7	4	5.5	839	93.2	5.90	32.25	20.35	26.30	4.322E6	2.847E7	1.639E7	100.000	40.755	70.377	6	1	4	0.0		0.0	Ankyrin repeat and BTB/POZ domain-containing protein 2 OS=Homo sapiens GN=ABTB2 PE=2 SV=1 - [ABTB2_HUMAN]

Q8TCE6	58.82	43.70	51.26	64	22	43	23	15	19	357	40.5	6.61	270.05	80.47	175.26	4.729E8	3.984E8	4.356E8	100.000	100.000	100.000	53	19	36	0.0	0.0	0.0	Protein FAM45A OS=Homo sapiens GN=FAM45A PE=2 SV=1 - [FA45A_HUMAN]
Q92609	50.57	31.95	41.26	162	99	130.5	43	25	34	795	88.9	6.54	636.70	372.09	504.39	5.700E8	4.670E8	5.185E8	100.000	30.024	65.012	118	67	93	0.0	58.6	29.3	TBC1 domain family member 5 OS=Homo sapiens GN=TBC1D5 PE=1 SV=1 - [TBCD5_HUMAN]
Q96L92	28.28	19.96	24.12	13	11	12	12	8	10	541	61.2	6.49	58.11	52.24	55.17	7.216E6	4.306E7	2.514E7	100.000	25.984	62.992	11	7	9	0.0	162.6	81.3	Sorting nexin-27 OS=Homo sapiens GN=SNX27 PE=1 SV=2 - [SNX27_HUMAN]
Q96NW4	45.14	6.19	25.67	51	5	28	35	5	20	1050	116.9	6.87	176.18	15.15	95.67	2.580E7	5.512E6	1.566E7	100.000	7.514	53.757	45	4	25	0.0	76.0	38.0	Ankyrin repeat domain-containing protein 27 OS=Homo sapiens GN=ANKRD27 PE=1 SV=2 - [ANR27_HUMAN]
Q96QK1	55.03	43.22	49.13	342	215	278.5	55	35	45	796	91.6	5.49	1498.02	868.06	1183.04	3.639E9	1.022E10	6.932E9	100.000	100.000	100.000	181	90	136	0.0	0.0	0.0	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]
Q9GZQ3	42.41	31.70	37.06	17	7	12	10	5	7.5	224	24.7	7.02	59.02	22.92	40.97	1.594E8	2.120E8	1.857E8	100.000	100.000	100.000	12	6	9	0.0	0.0	0.0	COMM domain-containing protein 5 OS=Homo sapiens GN=COMMD5 PE=1 SV=1 - [COMD5_HUMAN]
Q9H0A8	65.83	30.65	48.24	18	10	14	10	4	7	199	21.8	7.31	70.23	48.51	59.37	9.347E7	9.934E7	9.640E7	100.000	100.000	100.000	15	6	11	0.0	0.0	0.0	COMM domain-containing protein 4 OS=Homo sapiens GN=COMMD4 PE=1 SV=1 - [COMD4_HUMAN]
Q9HD34	28.57	37.36	32.97	3	4	3.5	2	4	3	91	10.8	10.73	14.72	13.85	14.28	2.544E6	6.147E6	4.345E6	50.641	6.785	28.713	2	4	3	132.9	21.3	77.1	LYR motif-containing protein 4 OS=Homo sapiens GN=LYRM4 PE=1 SV=1 - [LYRM4_HUMAN]
Q9NX08	53.01	48.63	50.82	13	9	11	8	6	7	183	21.1	5.43	57.84	40.38	49.11	1.254E8	1.220E8	1.237E8	100.000	100.000	100.000	11	8	10	0.0	0.0	0.0	COMM domain-containing protein 8 OS=Homo sapiens GN=COMMD8 PE=1 SV=1 - [COMD8_HUMAN]
Q9P000	45.96	68.69	57.33	20	21	20.5	8	9	8.5	198	21.8	5.88	81.45	71.23	76.34	2.455E8	1.687E8	2.071E8	100.000	78.387	89.194	15	15	15	0.0	37.3	18.7	COMM domain-containing protein 9 OS=Homo sapiens GN=COMMD9 PE=1 SV=2 - [COMD9_HUMAN]
Q9UBI1	55.90	53.33	54.62	18	17	17.5	9	8	8.5	195	22.1	5.99	77.22	65.24	71.23	1.811E8	1.706E8	1.758E8	100.000	100.000	100.000	13	16	15	0.0	0.0	0.0	COMM domain-containing protein 3 OS=Homo sapiens GN=COMMD3 PE=1 SV=1 - [COMD3_HUMAN]
Q9ULJ7	21.55	7.70	14.63	28	9	18.5	24	8	16	1429	155.8	6.60	111.11	46.07	78.59	5.846E6	1.749E7	1.167E7	100.000	13.787	56.894	26	9	18	0.0	401.5	200.8	Ankyrin repeat domain-containing protein 50 OS=Homo sapiens GN=ANKRD50 PE=1 SV=4 - [ANR50_HUMAN]
Q9Y5P4	7.85	12.18	10.02	4	8	6	4	6	5	624	70.8	5.48	19.20	33.71	26.46	1.188E6	2.152E7	1.136E7	28.113	4.100	16.106	4	7	6	578.4	3.7	291.0	Collagen type IV alpha-3-binding protein OS=Homo sapiens GN=COL4A3BP

PE=1 SV=1 -
[C43BP_HUMAN]